

REMARKS

Claims 1-2, 6-14, 16 and 28-33 are pending, upon entry of the amendment submitted above. Favorable reconsideration is respectfully requested.

Applicants would like to thank Examiner Fronda for the helpful and courteous discussion held with their representative on January 18, 2005 and a subsequent telephone discussion. During the discussions, the amendments presented above were discussed.

Applicants' representative also presented the Examiner with the results of the BLASTN search attached hereto. As noted on the Interview Summary form, the "BLASTN search results-shows significant alignments to coryneform bacterium citrate synthases."

At the discussion, the Examiner indicated that the amendments appear to place the application in condition for allowance, and that a final decision would be made after a written response was filed. The following remarks expand on the discussion with the Examiner.

The rejection under 35 U.S.C. §112, first paragraph, is believed to be obviated by the amendments submitted above.

Claim 1 has been amended to specify a citrate synthase gene obtained from *Corynebacterium glutamicum* or *Brevibacterium lactofermentum*. Claim 16 has been amended to specify that the citrate synthase gene is obtained from corynebacterium chromosomal DNA by the polymerase chain reaction using oligonucleotide primers of SEQ ID NO: 1 and SEQ ID NO: 2.

In view of those amendments, the results of the BLASTN search enclosed herewith and the disclosure of Eikmanns et al., Applicants had possession of the claimed subject at the time the present application was filed. Accordingly, the written description requirement is satisfied, and withdrawal of this ground of rejection is respectfully requested.

Application No. 09/419,611
Reply to Office Action of August 25, 2004

The rejection under 35 U.S.C. §112, second paragraph, is respectfully traversed.

Claim 11 has been amended to specify that the citrate synthase gene is obtainable by PCR amplification of chromosomal DNA using primers of SEQ ID NO: 1 and SEQ ID NO:

2. Claims 15 and 17 have been cancelled.

In view of the foregoing, the claims are definite within the meaning of 35 U.S.C. §112, second paragraph. Accordingly, withdrawal of this ground of rejection is respectfully requested.

Applicants submit that the present application is in condition for allowance. Early notice to this effect is earnestly solicited.

Respectfully submitted,

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MAIER & NEUSTADT, P.C.
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(OSMMN 06/04)

BLASTN Search Result

Computed at GenomeNet BLAST2 Server (Kyoto Center) on Thu Jan 6 11:07:20 JST 2005

Database Name NR-NT

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tblastn	prot	nucl
tblastx	nucl	nucl

BLASTN 2.2.10 [Oct-19-2004]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

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46,340,936 sequences; 80,264,366,952 total letters

Searching..... done

Sequences producing significant alignments:

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 Identities = 1308/1314 (99%)
 Strand = Plus / Plus

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Query: 121 aagatgctgtctgagactggactgatcactttgaccaggttatgtgaggactggctcc 180
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Query: 1141 gcaatggctcccaactgacttcttaccgtattttcgcaatcggtcgctgccagga 1200
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Query: 1201 tggatcgctcaactaccgcgaggcagctcggtcagcaggcaacaagatcaaccggccacgc 1260
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Query: 1261 caggtctacaccggcaaggaaatcccgaagttggcttcgtcgaggagcgctaa 1314
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>emb:BX927150 [BX927150] Corynebacterium glutamicum ATCC 13032, IS fingerprint type Top
4-5, complete genome; segment 3/10
Length = 348475

Score = 2557 bits (1290), Expect = 0.0
Identities = 1308/1314 (99%)
Strand = Plus / Plus

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Query: 61 ggcgagttcgaaatggacatcatcgaggcttctgaggtaacaacgggtttgtcctggc 120
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Query: 361 ctctggacgaggacttcaagtcccaagttcaacgttgtccacgcgacgctacccaaatg 420
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Sbjct: 181811 ctctggacgaggacttcaagtcccaagttcaacgttgtccacgcgacgctacccaaatg 181870

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Length = 3309401

Score = 2557 bits (1290), Expect = 0.0
Identities = 1308/1314 (99%)
Strand = Plus / Plus

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Query: 61 ggcgagttcgaaatggacatcatcgaggctctgaggtaacaacggtgttgcctggc 120
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Length = 1311

Top

Score = 2551 bits (1287), Expect = 0.0
Identities = 1305/1311 (99%)
Strand = Plus / Plus

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Query: 61 ggcgagttcgaaatggacatcatcgaggctctgagggtaacaacggtgttgcctggc 120
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Query: 421 gcaaccttggcttcgttaacatttgtctacccatcaccaggatcagctgaaccca 480
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Query: 481 ctcgatgaggcacagcttgataaggcaaccgttcgcctcatggcaaagggttccaatgctg 540
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Query: 721 aactgctccacccaccgttcgttatgtatcggttccgcacaggccaacatgtttgtctcc 780
Sbjct: 721 |||||||aactgctccacccaccgttcgttatgtatcggttccgcacaggccaacatgtttgtctcc 780

Query: 781 atcgctggtggcatcaacgcctgtccggcccactgcacggtgccaaaccaggctgtt 840
Sbjct: 781 |||||||atcgctggtggcatcaacgcctgtccggcccactgcacggtgccaaaccaggctgtt 840

Query: 841 ctggagatgctcgaagacatcaagaacaaccacggtgccgacgcacccgcgttcatgaac 900
Sbjct: 841 |||||||ctggagatgctcgaagacatcaagaaccacggtgccgacgcacccgcgttcatgaac 900

Query: 901 aaggtaagaacaaggaaagacggcgtccgcctcatgggttccgcacaccgcgtttacaag 960
Sbjct: 901 |||||||aaggtaagaacaaggaaagacggcgtccgcctcatgggttccgcacaccgcgtttacaag 960

Query: 961 aactacgatccacgtgcagcaatcgtaaggagaccgcacacgagatcctcgagcaccc 1020
Sbjct: 961 |||||||aactacgatccacgtgcagcaatcgtaaggagaccgcacacgagatcctcgagcaccc 1020

Query: 1021 ggtggcgacgatcttcgttatcgcaatcaagctgttgcacggaaattgcactggctgtat 1080
Sbjct: 1021 |||||||ggtggcgacgatcttcgttatcgcaatcaagctgttgcacggaaattgcactggctgtat 1080

Query: 1081 tacttcatctccgcagcttacccgaacgttagacttcatacccgcgttatcgatctaccgc 1140
Sbjct: 1081 |||||||tacttcatctccgcagcttacccgaacgttagacttcatacccgcgttatcgatctaccgc 1140

Query: 1141 gcaatggctcccaactgacttcttacccgtattgttcgttatcgcaatcggtcgctgccagg 1200
Sbjct: 1141 |||||||gcaatggctcccaactgacttcttacccgtattgttcgttatcgcaatcggtcgctgccagg 1200

Query: 1201 tggatcgctcaactaccgcgagcagctcggtgcaggcaggcaacaagatcaaccgcccacgc 1260
Sbjct: 1201 tggatcgctcaactaccgcgagcagctcggtgcaggcaggcaacaagatcaaccgcccacgc 1260

Query: 1261 caggtctacaccggcaaggaatcccgcaagttggttcctcgcgaggagcgc 1311
Sbjct: 1261 caggtctacaccggcaacgaatcccgcaagttggttcctcgcgaggagcgc 1311

>emb:AX123525 [AX123525] Sequence 3441 from Patent EP1108790.
Length = 1311



Score = 2551 bits (1287), Expect = 0.0
Identities = 1305/1311 (99%)
Strand = Plus / Plus

Query: 1 atgtttgaaaggatatcggtactgtataacaacaaggctgtcctgcactaccgg 60
Sbjct: 1 atgtttgaaaggatatcggtactgtataacaacaaggctgtcctgcactaccgg 60

Query: 61 ggcgagttcgaaatggacatcatcgaggcttctgaggtaacaacgggtttgtcctggc 120
Sbjct: 61 ggcgagttcgaaatggacatcatcgaggcttctgaggtaacaacgggtttgtcctggc 120

Query: 121 aagatgctgtcgactggactgtactttgaccaggatgtgaggactggctcc 180
Sbjct: 121 aagatgctgtcgactggactgtactttgaccaggatgtgaggactggctcc 180

Query: 181 accgagtcgaagatcacatcgatggcgatgcggaaatcctgcgttaccgcggctat 240
Sbjct: 181 accgagtcgaagatcacatcgatggcgatgcggaaatcctgcgttaccgcggctat 240

Query: 241 gacatcgctgatctggctgagaatgccaccaaactcaacgaggttttacctacttatcaac 300
Sbjct: 241 gacatcgctgatctggctgagaatgccaccaaactcaacgaggttttacctacttatcaac 300

Query: 301 ggtgaactaccaaccccgatgagcttcacaagttAACGACGAGATTGCCACCAACC 360
Sbjct: 301 ggtgagctaccaaccccgatgagcttcacaagttAACGACGAGATTGCCACCAACC 360

Query: 361 cttctggacgaggacttcaagtcccgatcaacgtgttccacgcgacgctacccatg 420
Sbjct: 361 cttctggacgaggacttcaagtcccgatcaacgtgttccacgcgacgctacccatg 420

Query: 421 gcaacccttggcttcctcggttaacattttgtctacctaaccaggatcagctgaaccca 480
Sbjct: 421 gcaacccttggcttcctcggttaacattttgtctacctaaccaggatcagctgaaccca 480

Query: 481 ctcgatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttcaatgctg 540
Sbjct: 481 ctcgatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttcaatgctg 540

Query: 541 gctgcgtacgcacaccgcgacgcaagggtgctcattacatgtacccagacaactccctc 600
Sbjct: 541 gctgcgtacgcacaccgcgacgcaagggtgctcattacatgtacccagacaactccctc 600

Query: 601 aacgcgcgtgagaacttcctgcgcatgatgttgcgttacccaaccgaggccatacgagatc 660
Sbjct: 601 aatgcgcgtgagaacttcctgcgcatgatgttgcgttacccaaccgaggccatacgagatc 660

Query: 661 gacccaatcatggtaaggctctggacaagctgcacgcgtgaccacgaggcag 720
Sbjct: 661 gacccaatcatggtaaggctctggacaagctgcacgcgtgaccacgaggcag 720

Query: 721 aactgctccacctccaccgttcgttatgatcggttccgcacaggccaaatgtttgtctcc 780
Sbjct: 721 aactgctccacctccaccgttcgttatgatcggttccgcacaggccaaatgtttgtctcc 780

Query: 781 atcgctggtggcatcaacgcgtctgtccggcccactgcacggggcggcaaccaggctgtt 840
Sbjct: 781 atcgctggtggcatcaacgcgtctgtccggcccactgcacggggcggcaaccaggctgtt 840

Query: 841 ctggagatgctcgaagacatcaagaacaaccacgtggcggcggcaaccgggtttcatgaac 900
Sbjct: 841 ctggagatgctcgaagacatcaagagacaaccacgtggcggcggcaaccgggtttcatgaac 900

Query: 901 aaggtaagaacaaggaagacggcggtccgcctcatggcttgcgttaccaag 960
Sbjct: 901 aaggtaagaacaaggaagacggcggtccgcctcatggcttgcgttaccaag 960

Query: 961 aactacgatccacgtgcagcaatgtcaaggagaccgcacacgagatcctcgagcacctc 1020
Sbjct: 961 aactacgatccacgtgcagcaatgtcaaggagaccgcacacgagatcctcgagcacctc 1020

Query: 1021 ggtggcgacgatcttctggatctggcaatcaagctggaaaggaaattgcactggctgtat 1080
Sbjct: 1021 ggtggcgacgatcttctggatctggcaatcaagctggaaaggaaattgcactggctgtat 1080

Query: 1081 tacttcatctcccgcaagcttacccgaacgttagacttctacaccggcgtatctaccgc 1140
Sbjct: 1081 tacttcatctcccgcaagcttacccgaacgttagacttctacaccggcgtatctaccgc 1140

Query: 1141 gcaatggctccaaactgacttctcaccgtattttcgcaatcggtcgctgccagga 1200
Sbjct: 1141 gcaatggctccaaactgacttctcaccgtattttcgcaatcggtcgctgccagga 1200

Query: 1201 tggatcgctactaccgcgaggcagctcggtgcagcaggcaacaagatcaaccggccacgc 1260
Sbjct: 1201 tggatcgctactaccgcgaggcagctcggtgcagcaggcaacaagatcaaccggccacgc 1260

Query: 1261 caggtctacaccggcaaggaaatcccgaagttggttcctcgcgaggagcgc 1311
Sbjct: 1261 caggtctacaccggcaacaatcccgaagttggttcctcgcgaggagcgc 1311

>gb:AP005217 [AP005217] *Corynebacterium efficiens* YS-314 DNA, complete genome, section 4/11.
Length = 300750



Top

Score = 1110 bits (560), Expect = 0.0
Identities = 1096/1273 (86%), Gaps = 5/1273 (0%)
Strand = Plus / Plus

Query: 3 gtttcaaaggatatacggtactgataacaacaaggctgtcctgcactacccgg 62
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 22750 gtttcaaaggatatacggtactgataacaacaaggctgtcactacccgg 22809

Query: 63 cgagttcgaaatggacatcatcgaggctctgaggtaacaacgggtttgtcctgg 122
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 22810 cgaattcgagatggcatcaagcaggccaccgaggtaactccgggtcatcctggtaa 22869

Query: 123 gatgctgtctgagactggactgatcacccgttatgtgagcactggctccac 182
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 22870 gatgctgtcgaaaccggctggcacccgttatgtcagcaccgggttcac 22929

Query: 183 cgagtcgaagatcacatcgatggcgatgggaatcctgcgttaccggctatga 242
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 22930 cgaatccaagatcacatcgatggtgatgcaggcatcctgcgtaccggctacga 22989

Query: 243 catcgctgatctggctgagaatgccacccatcgatggcgatgggaatcctgcgttaccctatcaacgg 302
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 22990 cattgcggatctggccggaaatgccacccatcgatggtgatgcaggcatcctgcgtatcaagg 23049

Query: 303 tgaactaccaaccccgatgagcttcacaagttAACGACGAGATTGCCACCCACCT 362
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 23050 ttagctcccggccggaaatgccacccatcgatggtgatgcaggcatcctgcgtaccacccct 23109

Query: 363 tctggacgaggacttcaagtcccgatcaacgtttccacgcgcacgtcacccatggc 422
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 23110 gctggacgaggacttcaagtcccgatcaatgtttccctcgatggccacccatggc 23169

Query: 423 aacccgtggcttcgttacatggatctactaccatcgaggatcagtcgtacccact 482
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 23170 caccctggcttcgttacatccctccaccatcgaggatcagtcgtggatccct 23229

Query: 483 cgatgaggcacagcttataaggcaaccgttcgcctcatggcaaagggttccatgtggc 542
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 23230 ggatgaggctcagtcggacaaggcaaccgtccgcgtatggcgaagggtccatgtggc 23289

Query: 543 tgctgtacgcacaccgcgcacgcaagggtgtccatgttacccatgttccatgtggc 602
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 23290 tgcatacgcacaccgtggcccaagggtgcgcgtatgttccatgttccatgtggc 23349

Query: 603 cgccgtgagaacttcctgcgtatgttccatgttccatgttccatgtggc 662
||||| ||||| ||||| ||||| ||||| ||||| |||||

Posted date: Jan 4, 2005 6:06 AM
Number of letters in database: 1,999,861,861
Number of sequences in database: 370,666

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.02
Posted date: Jan 4, 2005 6:13 AM
Number of letters in database: 1,999,963,845
Number of sequences in database: 360,118

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.03
Posted date: Jan 4, 2005 6:28 AM
Number of letters in database: 1,999,999,976
Number of sequences in database: 3,329,958

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.04
Posted date: Jan 4, 2005 6:45 AM
Number of letters in database: 1,999,999,708
Number of sequences in database: 3,404,633

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.05
Posted date: Jan 4, 2005 7:03 AM
Number of letters in database: 1,999,999,998
Number of sequences in database: 3,904,937

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.06
Posted date: Jan 4, 2005 7:23 AM
Number of letters in database: 1,999,999,553
Number of sequences in database: 4,328,864

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.07
Posted date: Jan 4, 2005 7:42 AM
Number of letters in database: 1,999,999,957
Number of sequences in database: 3,891,732

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.08
Posted date: Jan 4, 2005 7:59 AM
Number of letters in database: 1,999,999,671
Number of sequences in database: 3,486,474

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.09
Posted date: Jan 4, 2005 8:23 AM
Number of letters in database: 1,999,999,859
Number of sequences in database: 3,293,154

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.10
Posted date: Jan 4, 2005 8:41 AM
Number of letters in database: 1,999,999,669
Number of sequences in database: 3,828,471

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.11
Posted date: Jan 4, 2005 8:57 AM
Number of letters in database: 1,999,999,424
Number of sequences in database: 2,772,633

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.12
Posted date: Jan 4, 2005 9:05 AM
Number of letters in database: 1,999,921,952
Number of sequences in database: 631,119

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.13
Posted date: Jan 4, 2005 9:13 AM
Number of letters in database: 1,999,956,728
Number of sequences in database: 16,152

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.14

Posted date: Jan 4, 2005 9:19 AM
Number of letters in database: 1,999,893,819
Number of sequences in database: 9139

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.15
Posted date: Jan 4, 2005 9:25 AM
Number of letters in database: 1,999,809,626
Number of sequences in database: 8148

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.16
Posted date: Jan 4, 2005 9:32 AM
Number of letters in database: 1,999,958,517
Number of sequences in database: 9281

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.17
Posted date: Jan 4, 2005 9:39 AM
Number of letters in database: 1,999,869,985
Number of sequences in database: 118,685

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.18
Posted date: Jan 4, 2005 9:46 AM
Number of letters in database: 1,999,869,072
Number of sequences in database: 575,666

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.19
Posted date: Jan 4, 2005 9:55 AM
Number of letters in database: 1,999,866,894
Number of sequences in database: 705,081

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.20
Posted date: Jan 4, 2005 10:02 AM
Number of letters in database: 1,999,925,325
Number of sequences in database: 63,082

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.21
Posted date: Jan 4, 2005 10:10 AM
Number of letters in database: 1,999,999,826
Number of sequences in database: 569,309

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.22
Posted date: Jan 4, 2005 10:22 AM
Number of letters in database: 1,997,416,774
Number of sequences in database: 2,119,519

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.23
Posted date: Jan 4, 2005 10:29 AM
Number of letters in database: 1,999,944,509
Number of sequences in database: 107,016

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.24
Posted date: Jan 4, 2005 10:36 AM
Number of letters in database: 1,999,998,745
Number of sequences in database: 293,074

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.25
Posted date: Jan 4, 2005 10:45 AM
Number of letters in database: 1,999,996,900
Number of sequences in database: 1,064,738

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.26
Posted date: Jan 4, 2005 10:55 AM
Number of letters in database: 1,999,992,337
Number of sequences in database: 933,438

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.27

Posted date: Jan 4, 2005 11:02 AM
Number of letters in database: 1,999,979,685
Number of sequences in database: 288,812

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt. 28
Posted date: Jan 4, 2005 11:09 AM
Number of letters in database: 1,999,992,360
Number of sequences in database: 288,789

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt. 29
Posted date: Jan 4, 2005 11:16 AM
Number of letters in database: 1,999,991,524
Number of sequences in database: 89,111

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt. 30
Posted date: Jan 4, 2005 11:23 AM
Number of letters in database: 1,999,976,519
Number of sequences in database: 217,802

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt. 31
Posted date: Jan 4, 2005 11:29 AM
Number of letters in database: 1,999,995,610
Number of sequences in database: 136,831

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt. 32
Posted date: Jan 4, 2005 11:36 AM
Number of letters in database: 1,999,921,996
Number of sequences in database: 162,607

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt. 33
Posted date: Jan 4, 2005 11:43 AM
Number of letters in database: 1,999,964,690
Number of sequences in database: 218,162

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt. 34
Posted date: Jan 4, 2005 11:50 AM
Number of letters in database: 1,999,976,965
Number of sequences in database: 61,666

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt. 35
Posted date: Jan 4, 2005 11:57 AM
Number of letters in database: 1,999,991,196
Number of sequences in database: 368,188

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt. 36
Posted date: Jan 4, 2005 12:05 PM
Number of letters in database: 1,999,904,998
Number of sequences in database: 477,581

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt. 37
Posted date: Jan 4, 2005 12:11 PM
Number of letters in database: 1,999,925,109
Number of sequences in database: 63,652

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt. 38
Posted date: Jan 4, 2005 12:18 PM
Number of letters in database: 1,999,998,888
Number of sequences in database: 310,761

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt. 39
Posted date: Jan 4, 2005 12:25 PM
Number of letters in database: 1,998,257,110
Number of sequences in database: 177,152

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt. 40

Posted date: Jan 4, 2005 12:26 PM
Number of letters in database: 270,246,158
Number of sequences in database: 39,235

Lambda K H
1.37 0.711 1.31

Gapped
Lambda K H
1.37 0.711 1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 36,390,912
Number of Sequences: 46340936
Number of extensions: 36390912
Number of successful extensions: 627339
Number of sequences better than 10.0: 220
Number of HSP's better than 10.0 without gapping: 220
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 624290
Number of HSP's gapped (non-prelim): 3035
length of query: 1314
length of database: 80,264,366,952
effective HSP length: 24
effective length of query: 1290
effective length of database: 79,152,184,488
effective search space: 102106317989520
effective search space used: 102106317989520
T: 0
A: 0
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 22 (44.1 bits)

=

BLASTP Search Result

Computed at GenomeNet BLAST2 Server (Kyoto Center) on Thu Jan 6 11:02:36 JST 2005

Database Name NR-AA

>query

```
MFERDIVATD NNKAVLHYPG GEFEMDIIEA SEGNNNGVVLG KMLSETGLIT
FDPGYVSTGS TESKITYIDG DAGILRYRGY DIADLAENAT FNEVSYLLIN
GELPTPDELH KFNDEIRHHT LLDEDFKSQF NVFPRDAHPM ATLASSVNIL
STYYQDQLNP LDEAQLDKAT VRLMAKVPML AAYAHRARKG APYMPDNSL
NARENFLRMM FGYPTEPYE I DPIMVKALDK LLILHADHEQ NCSTSTVRMI
GSAQANMFVS IAGGINALSG PLHGGGANQAV LEMLEDIKNN HGGDATAFMN
KVKNKEDGVR LMGFGRVYK NYDPRAAIVK ETAHEILEHL GGDDLLLALI
KLEELIALADD YFISRKLYPN VDFYTGLIYR AMGFPTDFFT VLFAIGRLPG
WIAHYREQLG AAGNKINRPR QVYTGKESRK LPREER*
```

BLASTP 2.2.10 [Oct-19-2004]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= query
(437 letters)

Database: nr-aa: Non-redundant protein sequence database Release
05-01-04
1,848,798 sequences; 600,567,511 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
---	-----------------	------------

<input checked="" type="checkbox"/> Top 10 <input type="button" value="Clear"/> <input type="button" value="Select operation"/> <input type="button" value="Exec"/>	Score (bits)	E Value
<input checked="" type="checkbox"/> sp:CISY_CORGL [P42457] Citrate synthase (EC 2.3.3.1).>pir:I40717...	855	0.0
<input checked="" type="checkbox"/> gp:AX065419_1 [AX065419] Sequence 545 from Patent WO0100844. [Co...	842	0.0
<input checked="" type="checkbox"/> tr:Q8RQP3 [Q8RQP3] Citrate synthase (EC 2.3.3.1).>gpu:BA000035_9...	798	0.0
<input checked="" type="checkbox"/> tr:Q6NIJ0 [Q6NIJ0] Citrate synthase (EC 2.3.3.1).>trnew:CAE49303...	750	0.0
<input checked="" type="checkbox"/> tr:Q9RMRO [Q9RMRO] Citrate synthase.>gp:AF191033_1 [AF191033] ci...	548	e-155
<input checked="" type="checkbox"/> tr:Q5Z238 [Q5Z238] Putative citrate synthase.>gpu:AP006618_661 [...]	546	e-154
<input checked="" type="checkbox"/> tr:Q9R339 [Q9R339] Citrate synthase (EC 4.1.3.7).>gpu:SC0939113_...	536	e-151
<input checked="" type="checkbox"/> tr:Q7U122 [Q7U122] PROBABLE CITRATE SYNTHASE I GLTA2 (EC 2.3.3.1...)	535	e-150
<input checked="" type="checkbox"/> sp:CISY_MYCTU [Q10530] Citrate synthase 1 (EC 2.3.3.1).>pir:E707...	535	e-150
<input checked="" type="checkbox"/> tr:Q82CL5 [Q82CL5] Putative citrate synthase.>gpu:BA000030_5334 ...	533	e-150

>sp:CISY_CORGL [P42457] Citrate synthase (EC 2.3.3.1).>pir:I40717 [I40717] citrate 
(si)-synthase (EC 4.1.3.7) - Corynebacterium
glutamicum>prf:2106273A citrate synthase -
Corynebacterium glutamicum>gpu:BA000036_829 [BA000036]
Citrate synthase [Corynebacterium glutamicum ATCC 13032]
Length = 437

Score = 855 bits (2209), Expect = 0.0
Identities = 425/437 (97%), Positives = 426/437 (97%)

Query: 1 MFERDIVATDNNKAVLHYPGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGS 60
 MFERDIVATDNNKAVLHYPGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGS
 Sbjct: 1 MFERDIVATDNNKAVLHYPGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGS 60

Query: 61 TESKITYIDGDAGILRYRGYDIAADLAENATFNEVSYLLINGELPTPDELHKFNDEIRHHT 120
 TESKITYIDGDAGILRYRGYDIAADLAENATFNEVSYLLINGELPTPDELHKFNDEIRHHT
 Sbjct: 61 TESKITYIDGDAGILRYRGYDIAADLAENATFNEVSYLLINGELPTPDELHKFNDEIRHHT 120

Query: 121 LLDEDFKSQNFVPRDAHPMATLASSVNILSTYYQDQLNPLDEAQLDKATVRLMAKVPML 180
 LLDEDFKSQNFVPRDAHPMATLASSVNILSTYYQDQLNPLDEAQLDKATVRLMAKVPML
 Sbjct: 121 LLDEDFKSQNFVPRDAHPMATLASSVNILSTYYQDQLNPLDEAQLDKATVRLMAKVPML 180

Query: 181 AAYAHRARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQ 240
 AAYAHRARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQ
 Sbjct: 181 AAYAHRARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQ 240

Query: 241 NCSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDKNNHGGDATAFMN 300
 NCSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDK-NHGGDAT FMN
 Sbjct: 241 NCSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDKSNHGGDATEFMN 300

Query: 301 KVKNKEDGVRLMGFGHRYKNYDPRAAIVKETAHEILEHXXXXXXXXXAIKLEEIALADD 360
 KVKNKEDGVRLMGFGHRYKNYDPRAAIVKETAHEILEH AIKLEEIALADD
 Sbjct: 301 KVKNKEDGVRLMGFGHRYKNYDPRAAIVKETAHEILEHLGGDDLLDLAIKLEEIALADD 360

Query: 361 YFISRKLYPNVDFTYTGILYRAMGFTDFTVLFAGRLPGWIAHYREQLGAAGNKINRPR 420
 YFISRKLYPNVDFTYTGILYRAMGFTDFTVLFAGRLPGWIAHYREQLGAAGNKINRPR
 Sbjct: 361 YFISRKLYPNVDFTYTGILYRAMGFTDFTVLFAGRLPGWIAHYREQLGAAGNKINRPR 420

Query: 421 QVYTGKESRKLVPREER 437
 QVYTG ESRKLVPREER
 Sbjct: 421 QVYTGNESRKLVPREER 437

>gp:AX065419_1 [AX065419] Sequence 545 from Patent WO0100844. [Corynebacterium [▲ Top](#)
glutamicum]
 Length = 431

Score = 842 bits (2175), Expect = 0.0
 Identities = 418/431 (96%), Positives = 420/431 (97%)

Query: 7 VATDNNKAVLHYPGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT 66
 +ATDNNKAVLHYPGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT
 Sbjct: 1 MATDNNKAVLHYPGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT 60

Query: 67 YIDGDAGILRYRGYDIAADLAENATFNEVSYLLINGELPTPDELHKFNDEIRHHTLLDEF 126
 YIDGDAGILRYRGYDIAADLAENATFNEVSYLLINGELPTPDELHKFNDEIRHHTLLDEF
 Sbjct: 61 YIDGDAGILRYRGYDIAADLAENATFNEVSYLLINGELPTPDELHKFNDEIRHHTLLDEF 120

Query: 127 KSQNFVPRDAHPMATLASSVNILSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYAHR 186
 KSQNFVPRDAHPMATLASSVNILSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYAHR
 Sbjct: 121 KSQNFVPRDAHPMATLASSVNILSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYAHR 180

Query: 187 ARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTST 246
 ARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTST
 Sbjct: 181 ARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTST 240

Query: 247 VRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDKNNHGGDATAFMNKVKNKE 306
 VRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDK-NHGGDAT FMNKVKNKE
 Sbjct: 241 VRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDKSNHGGDATEFMNKVKNKE 300

Query: 307 DGVRLMGFGRVYKNYDPRAAIVKETAHEILEHXXXXXXXXXAIKLEEIALADDYFISRK 366
 DGVRLMGFGRVYKNYDPRAAIVKETAHEILEH AIKLEEIALADDYFISRK
 Sbjct: 301 DGVRLMGFGRVYKNYDPRAAIVKETAHEILEHLGGDDLLDLAIKLEEIALADDYFISRK 360

Query: 367 LYPNVDFYTGLIYRAMGFTDFFTTLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGK 426
 LYPNVDFYTGLIYRAMGFTDFFTTLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTG
 Sbjct: 361 LYPNVDFYTGLIYRAMGFTDFFTTLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGN 420

Query: 427 ESRKLVPREER 437
 ESRKLVPREER
 Sbjct: 421 ESRKLVPREER 431

>tr:Q8RQP3 [Q8RQP3] Citrate synthase (EC 2.3.3.1).>gpu:BA000035_903 [BA000035] ▲Top
 citrate synthase [Corynebacterium efficiens
 YS-314]>gp:AB082520_1 [AB082520] citrate synthase
 [Corynebacterium efficiens]>gp:AP005217_19 [AP005217]
 citrate synthase [Corynebacterium efficiens YS-314]
 Length = 470

Score = 798 bits (2060), Expect = 0.0
 Identities = 394/436 (90%), Positives = 413/436 (94%), Gaps = 1/436 (0%)

Query: 2 FERDIVATDNNKAVLHYPGGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGST 61
 FER+IVA+DNNKAVLHYPGGEFEM I+A+EGN+GV+LGKMLSETGL+TFDPGYVSTGST
 Sbjct: 36 FEREIVASDNNKAVLHYPGGEFEMGIKQATEGNSGVLGKMLSETGLVTFDPGYVSTGST 95

Query: 62 ESKITYIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTPDELHKFNDEIRHHTL 121
 ESKITYIDGDAGILRYRGYDIADLAENATFNEVSYLLI GELPTP+ELHKFNDEIRHHTL
 Sbjct: 96 ESKITYIDGDAGILRYRGYDIADLAENATFNEVSYLLIKGELPTPEELHKFNDEIRHHTL 155

Query: 122 LDEDFKSQFNVFPRDAHPMATLASSVNILSTYYQDQLNPLDEAQLDKATVRLMAKVPMLA 181
 LDEDFKSQFNVFPRDAHPMATLASSVNILSTYYQDQL+PLDEAQLDKATVRLMAKVPMLA
 Sbjct: 156 LDEDFKSQFNVFPRDAHPMATLASSVNILSTYYQDQLPDLDEAQLDKATVRLMAKVPMLA 215

Query: 182 AYAHRAKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQN 241
 AYAHRAKGAPYMPDNSLNARENFLRMMFGYPTEPYE+DPIMVKALDKLLILHADHEQN
 Sbjct: 216 AYAHRAKGAPYMPDNSLNARENFLRMMFGYPTEPYEVDPIMVKALDKLLILHADHEQN 275

Query: 242 CSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNHGGDATAFMNK 301
 CSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLE+I N GGDAT FMN+
 Sbjct: 276 CSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLELEEIAAN-GGDATDFMNR 334

Query: 302 VKNKEGVRLMGFGHRVYKNYDPRAAIVKETAHEILEHXXXXXXXXXIKLEEIALADDY 361
 VKNKE GVRLMGFGHRVYKNYDPRAAIVK+TAHEILEH A+KLEEIAL DDY
 Sbjct: 335 VKNKEGVRLMGFGHRVYKNYDPRAAIVKDTAHEILEHLGGDPPLDLALKLEEIALNDDY 394

Query: 362 FISRKLYPNVDFYTGLIYRAMGFTDFFTTLFAIGRLPGWIAHYREQLGAAGNKINRPRQ 421
 FISRKLYPNVDFYTGLIYRAMGFTDFFTTLFAIGRLPGWIAHYREQL G KINRPRQ
 Sbjct: 395 FISRKLYPNVDFYTGLIYRAMGFTDFFTTLFAIGRLPGWIAHYREQLADPGAKINRPRQ 454

Query: 422 VYTGKESRKLVPREER 437
 +YTG+ +RK++PREER
 Sbjct: 455 IYTGETARKIIIPREER 470

>tr:Q6NIJ0 [Q6NIJ0] Citrate synthase (EC 2.3.3.1).>trnew:CAE49303 [CAE49303] ▲Top
 Citrate synthase (EC 2.3.3.1).>gpu:BX248356_61
 [BX248356] citrate synthase [Corynebacterium
 diphtheriae]>gp:BX248356_61 [BX248356] citrate synthase
 [Corynebacterium diphtheriae]
 Length = 435

Score = 750 bits (1937), Expect = 0.0
 Identities = 371/433 (85%), Positives = 401/433 (92%), Gaps = 3/433 (0%)

Query: 6 IVATDN-NKAVLHYPGGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESK 64

+VAT+N +KAVLHYPGGE+EMDII A+EGN+GVVL K+LS+TG++TFDPGYVSTGSTESK
 Sbjct: 5 LVATENKDKAVLHYPGGEYEMDI IHATEGNDGVLDKLLSQTMVTFDPGYVSTGSTESK 64

Query: 65 ITYIDGDAGILRYRGYDIADLAENATFNEVSILLINGELPTPDELHKFNDEIRHHTLLDE 124
 ITYIDGD GILR+RGYDIADLAENATFNEVSILLI G LPT DELHKFN+EIRHHTLLDE
 Sbjct: 65 ITYIDGDNGILRHRYGYDIADLAENATFNEVSILLIKGHLPTVDELHKFNNEIRHHTLLDE 124

Query: 125 DFKSQFNVFPRDAHPMATLASSVNILSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYA 184
 DFKSQFN+FPRDAHPM+ LASSVNILSTYYQDQLNPLDE QLDKATVRL+AKVPMLAAYA
 Sbjct: 125 DFKSQFNIFPRDAHPMSVLASSVNILSTYYQDQLNPLDEEQLDKATVRLAKVPMLAAYA 184

Query: 185 HRARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCST 244
 +RA KGAPYMPDNSLNARENFLRMMFGYPTEPYE+DP++ KALDKLLILHADHEQNCST
 Sbjct: 185 YRASKGAPYMPDNSLNARENFLRMMFGYPTEPYEVDPVVAKALDKLLILHADHEQNCST 244

Query: 245 STVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNHHGGDATAFMNKVKN 304
 STVRMIGSAQANMFV++AGGINALSGPLHGGANQAVLEMLE+IK N GGDAT FMN+VKN
 Sbjct: 245 STVRMIGSAQANMFVAVAGGINALSGPLHGGANQAVLEMLEEIKAN-GGDATDFMNDRVKN 303

Query: 305 KEDGVRLMGFGHRVYKNYDPRAAIVKETAHEILEHXXXXXXXXXAIKLEEIALADDYFIS 364
 KE GVRLMGFGHRVYKNYDPRAAIVKETAHEILEH A+KLEEIAL+DDYF+S
 Sbjct: 304 KEKGVRLMGFGHRVYKNYDPRAAIVKETAHEILEH LGGDELLDLAMKLEEALSDDYFVS 363

Query: 365 RKLYPNVDFYTGLIYRAMGFPTDFFTTLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYT 424
 RKLYPNVDFYTGLIYRAMGFPTDFFTTLFAIGRLPGWIA YREQL A KINRPRQ+YT
 Sbjct: 364 RKLYPNVDFYTGLIYRAMGFPTDFFTTLFAIGRLPGWIAQYREQL-ATTTKINRPRQIYT 422

Query: 425 GKESRKLVPREER 437
 G+ RK+ PRE+R
 Sbjct: 423 GETLRKVTPREQR 435

>tr:Q9RMRO [Q9RMRO] Citrate synthase. >gp:AF191033_1 [AF191033] citrate synthase [Mycobacterium smegmatis] ▲Top
 Length = 441

Score = 548 bits (1413), Expect = e-155
 Identities = 272/421 (64%), Positives = 328/421 (77%), Gaps = 2/421 (0%)

Query: 18 YPGGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKITYIDGDAGILRY 77
 YPGG+ E+ I+A+EG + V LGK L+ET L TFD G+++T ST+S ITYIDG+ GILRY
 Sbjct: 22 YPGKLELPILKATEGTDSVALGKFLAETNLTFDSGMNTASTKSITYIDGEQQGILRY 81

Query: 78 RGYDIADLAENATFNEVSILLINGELPTPDELHKFNDEIRHHTLLDEDFKSQFNVFPRDA 137
 RG I LAE +TF EVSILLI GELPTP +L +F +I+ HTLL ED K F+ FPR+A
 Sbjct: 82 RGIPIEQLAEKSTFIEVSILLIYGELPTPTQLEEFFTKIQRHTLLHEDLKRFFDGFPRNA 141

Query: 138 HPMATLASSVNILSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYAHARKGAPYMPD 197
 HPM L+S+VN LS YYQD L+P D+ Q++ +T+RL+AK+P +AAYA++ G P++YPD
 Sbjct: 142 HPMPVLSSAVNALSAKYQDSLDPKDDEQVELSTIRLLAKLPTIAAYAKKSAGQPFLYPD 201

Query: 198 NSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTSTVRMIGSAQANM 257
 NSL+ ENFLRM FG+P EPYE++P + KALD L ILHADHEQNCSTSTVR++GS+QAN+
 Sbjct: 202 NSLSLVENFLRMTFGFPAAEPYEVNPDVAKALDMLFILHADHEQNCSTSTVRLVGSSQANL 261

Query: 258 FVSIAGGINALSGPLHGGANQAVLEMLEDIKNHHGGDATAFMNKVKNKEDGVRLMGFGR 317
 F SI+GGINAL GPLHGGANQAVLEML+ IK + GGD FM +VKNKE GV+LMGFGHR
 Sbjct: 262 FTSISGGINALWGPLHGGANQAVLEMLDAIKAD-GGDTKKFMERVKNKAEAVKLMGFGHR 320

Query: 318 VYKNYDPRAAIVKETAHEILEHXXXXXXXXXAIK-LEEIALADDYFISRKLYPNVDFYTG 376
 VYKNYDPRAAIVK+TA +ILE K LEE+AL DDYF I RKLYPNVDFYTG
 Sbjct: 321 VYKNYDPRAAIVKKTADQILETLGVQDDLLEIAKGLEEVALNDDYFIERKLYPNVDFYTG 380

Query: 377 LIYRAMGFPTDFFTTLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGESRKLVPREE 436

+IYRAMGFPT FTVLFA+GRLPGWIAH+RE KI RPRQ+YTG R VP +
 Sbjct: 381 VIYRAMGFPTRMFTVLFALGRLPGWIAHWREMHDPTTKIGRPRQLYTGYTERDYVPMSD 440

Query: 437 R 437
 R
 Sbjct: 441 R 441

>tr:Q5Z238 [Q5Z238] Putative citrate synthase. >gpu:AP006618_661 [AP006618] ▲Top
 putative citrate synthase [Nocardia farcinica IFM
 10152]>gp:AP006618_661 [AP006618] putative citrate
 synthase [Nocardia farcinica]
 Length = 433

Score = 546 bits (1406), Expect = e-154
 Identities = 270/421 (64%), Positives = 328/421 (77%), Gaps = 3/421 (0%)

Query: 10 DNNKAVLHYPGGEFEMDI IEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKITYID 69
 D+ K VL YPGGE+ M I EA+EGN+G+ LGKML+ TG +T+DPG+++T T+S ITYID
 Sbjct: 7 DDAKPVLSPYGGEYAMTI TEATEGNHGIDLGKMLASTGYVTYDPGFMNTAPTKSAITYID 66

Query: 70 GDAGILRYRGYDADLAENATFNEVSYLLINGELPTPDELHKFNDEIRHHTLLDEDFKSQ 129
 G+AGILRYRGY I LA+++TF EVSYLLI GELPT +L F D IR HTLL ED K
 Sbjct: 67 GEAGILRYRGYPIEQLADSSTFIEVSYLLIYGELPTQAQLDDFTDRIRRHTLLHEDLKRF 126

Query: 130 FNVFPRDAHPMATLASSVNILSTYYQDQLNPLDEAQLDKATVRLMAKVPMIAAYHRARK 189
 F+ FPR+AHPM L+S+VN LS YYQD L+P D Q++ +T+RL+AK+P +AAY+++
 Sbjct: 127 FDGFPNAHPMPVLSAVNALSAYYQDSLDPDPEQVELSTIRLLAKLPTIAAYSYKKSV 186

Query: 190 GAPYMPDNLNARENFLRMMFGYPTEPYIEDPIMVKALDKLLILHADHEQNCSTSTVRM 249
 G P++YPDNSL ENFLRM FG+P EPYE+DP + ALD LLILHADHEQNCSTSTVR+
 Sbjct: 187 GQPFLYPDNLTLVENFLRMTFGFPAEPYEVDPPEVAALDMILLIHADHEQNCSTSTVR 246

Query: 250 IGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKNKEDGV 309
 +GS+ AN+F S++GGINAL GPLHGGANQAVLEML+DIK GGD F+ KVKNKEDGV
 Sbjct: 247 VGSSDANLFTS VSGGINALWGPLHGGANQAVLEMDDIK-AQGGDVKEFIRKVKNKEDGV 305

Query: 310 RLMGFGHRVYKNYDPRAAIVKETAHEILEH-XXXXXXXXXIKLEEIALADDYFISRKLY 368
 +LMGFGHRVY+NYDPRAAI K+ A IL A LEE AL DDYF+ R+LY
 Sbjct: 306 KLMGFGHRVYRNYPRAAIKKHADNILRKLGDDDELFEIAQALEAAALTDDYFVERRLY 365

Query: 369 PNVDFYTGIIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGKES 428
 PNVDFYTG+IY+AMGFPT FTVLFA+GRLPGWIAH+RE + + KI RPRQ+YTG +
 Sbjct: 366 PNVDFYTGVIYKAMGFPTRMFTVLFAMGRLPGWIAHWRE-MHSEPLKIGRPRQIYTGYGA 424

Query: 429 R 429
 R
 Sbjct: 425 R 425

>tr:Q9R339 [Q9R339] Citrate synthase (EC 4.1.3.7). >gpu:SC0939113_211 ▲Top
 [AL939113] citrate synthase. [Streptomyces coelicolor
 A3(2)]>gp:SC0939113_211 [AL939113] citrate synthase.
 [Streptomyces coelicolor A3(2)]>gp:AF181118_1 [AF181118]
 citrate synthase [Streptomyces coelicolor]
 Length = 429

Score = 536 bits (1382), Expect = e-151
 Identities = 265/428 (61%), Positives = 327/428 (76%), Gaps = 2/428 (0%)

Query: 11 NNKAVLHYPGGEFEMDI IEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKITYIDG 70
 +N VL Y GE+ +I+++ G+ G +GK+ ++TGL+T D GY +T + +S ITY+DG
 Sbjct: 3 DNSVVLRYGDGEYTYPVIDSTVGDKGFDIGKLRAQTGLVTLDSGYGNTAAYKSAITYLDG 62

Query: 71 DAGILRYRGYDIADLAENATFNEVSYLLINGELPTPDELHKFNDEIRHHTLLDEFKSQF 130
+AGILRYRGY I LAE ++F EV+YLLINGELPT DEL F EI HTLL ED K+ +
Sbjct: 63 EAGILRYRGYPIEQLAERSSFVEVAYLLINGELPTVDELSAFKGEITQHTLLHEDVKNFY 122

Query: 131 NVFPRDAHPMATLASSVNILSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYAHRARKG 190
FPRDAHPMA L+S V+ LST+YQD NP DE Q + +T+RL+AK+P +AAYA++ G
Sbjct: 123 KGFPFRDAHPMAMLSVSVSALSTFYQDSHNPFDERRQRNLSTIRLLAKLPTIAAYAYKKSIG 182

Query: 191 APYMPDNSLNARENFLRMFMGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTSTVRMI 250
P++YP N+L ENFLRM F P + YE+DP +V ALDKLLILHADHEQNCSTSTVR++
Sbjct: 183 HPFVYPANNLGYVENFLRMTFSVPAQEYELDPTVVAALDKLLILHADHEQNCSTSTVRLV 242

Query: 251 GSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEIDKNHHGGDATAFMNKVKNKEGV 310
GS+QANMF SI+ GINAL GPLHGGANQ+VLEMLE I+ + GGD +F+ KVKNKEGV
Sbjct: 243 GSSQANMFASISAGINALWGPLHGGANQSVLEMLEGIR-DAGGDVDSFIRKVKNKEGV 301

Query: 311 LMGFGHRVYKNYDPRAAIVKETAHEILEH-XXXXXXXXXIKLEEIALADDYFISRKL 369
LMGFGHRVYKN+DPRA I+K AH++L A+KLEE AL+DDYF+SR L 361
Sbjct: 302 LMGFGHRVYKNFDPRAKIKAAGHDVLSALGKSDLELLIAALKLEEHALSDDYFVSRSL 361

Query: 370 NVDFTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGKESR 429
NVDFTGLIYRAMGFPT+FTVLFA+GRLPGWIA+E+G++I RPRQ+YTG R
Sbjct: 362 NVDFTGLIYRAMGFTEMFTVLFALGRLPGWIAQWHEMIKEPGSRIGRPRQIYTGVVER 421

Query: 430 KLVPREER 437
VP EER
Sbjct: 422 DFVPVEER 429

>tr:Q7U122 [Q7U122] PROBABLE CITRATE SYNTHASE I GLTA2 (EC
2.3.3.1). >gp:BX248337_9 [BX248337] PROBABLE CITRATE
SYNTHASE I GLTA2 [Mycobacterium bovis AF2122/97]
Length = 431

[▲Top](#)

Score = 535 bits (1377), Expect = e-150
Identities = 264/432 (61%), Positives = 326/432 (75%), Gaps = 2/432 (0%)

Query: 7 VATDNNKAVLHYPGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT 66
+A ++ A L YPGGE ++ I+ A+EG +G+ LG +L++TG TFD G+ +T + +S IT
Sbjct: 1 MADTDDTATLRYPGGEIDLQIVHATEGADGIALGPLLAKTGHTTFDVGFANTAAKSSIT 60

Query: 67 YIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTPDELHKFNDEIRHHTLLDEF 126
YIDGDAGILRYRGY I LAE +TF EV YLLI GELP D+L +F I+ HT+L ED
Sbjct: 61 YIDGDAGILRYRGYPIDQLAEKSTFIEVCYLLIYGELPDTDQLAQFTGRQRHTMLHEDL 120

Query: 127 KSQFNVFPRDAHPMATLASSVNILSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYAHR 186
K F+ FPR+AHPM L+S VN LS YYQD L+P+D Q++ +T+RL+AK+P +AAYA++
Sbjct: 121 KRFFDGFPNAHPMPVLSSVNVNALSAYQDALPMNDNGQVELSTIRLLAKLPTIAAYAYK 180

Query: 187 ARKGAPYMPDNSLNARENFLRMFMGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTST 246
G P++YPDNSL ENFLR+ FG+P EPY+ DP +V+ALD L ILHADHEQNCSTST
Sbjct: 181 KSVGQPFLYPDNSLTIVENFLRLTFGFPQAEPYQADPEVVRALDMLFILHADHEQNCSTST 240

Query: 247 VRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEIDKNHHGGDATAFMNKVKNKE 306
VR++GS++AN+F SI+GGINAL GPLHGGANQAVLEMLE I+++ G D + F+ KVKN+E
Sbjct: 241 VRLVGSSRANLFTSISGGINALWGPLHGGANQAVLEMLEGIRDS-GDDVSEFVRVKVNRE 299

Query: 307 DGVRLMGFGRVYKNYDPRAAIVKETAHEILEHXXXXXXXXXIK-LEEIALADDYFISR 365
GV+LMGFGHRVYKNYDPRA IVKE A +IL K LEE AL DDYF I R
Sbjct: 300 AGVKLMGFGRVYKNYDPRAVIKEQADKILAKLGDDSSLGIAKELEEAALTDDYFIER 359

Query: 366 KLYPNVDFTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTG 425
KLYPNVDFTGLIYRA+GFT FTVLFA+GRLPGWIAH+RE +KI RPRQ+YTG
Sbjct: 360 KLYPNVDFTGLIYRALGFPTRMFTVLFALGRLPGWIAHWREMHDGDSKIGRPRQIYTG 419

Query: 426 KESRKLVPREER 437
 R V + R
 Sbjct: 420 YAERDYVTIDAR 431

>sp:CISY_MYCTU [Q10530] Citrate synthase 1 (EC 2.3.3.1).>pir:E70782 [E70782] ▲Top
 probable gltA2 protein - Mycobacterium tuberculosis
 (strain H37RV)>gp:AE000516_946 [AE000516] citrate
 synthase [Mycobacterium tuberculosis
 CDC1551]>gp:BX842574_319 [BX842574] PROBABLE CITRATE
 SYNTHASE I GLTA2 [Mycobacterium tuberculosis H37Rv]
 Length = 431

Score = 535 bits (1377), Expect = e-150
 Identities = 264/432 (61%), Positives = 326/432 (75%), Gaps = 2/432 (0%)

Query: 7 VATDNNKAVLHYPGGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT 66
 +A ++ A L YPGGE ++ I+ A+EG +G+ LG +L++TG TFD G+ +T + +S IT
 Sbjct: 1 MADTDDTATLRYPGGEIDLQIVHATEGADGI ALGPLLAKTGHTTFDVGFA NTAAKSSIT 60

Query: 67 YIDGDAGILRYRGYDIAADLAENATFNEVSYLLINGELPTPDELHKFNDEIRHHTLLDED 126
 YIDGDAGILRYRGY I LAE +TF EV YLLI GELP D+L +F I+ HT+L ED
 Sbjct: 61 YIDGDAGILRYRGYPIDQLAEKSTFIEVCYLLIYGELPDTDQLAQFTGRQRHMLHEDL 120

Query: 127 KSQFNVFPRDAHPMATLASSVNILSTYYQDQLNPLDEAQLDKATVRLMAKVPMIAAYAH 186
 K F+ FPR+AHPM L+S VN LS YYQD L+P+D Q++ +T+RL+AK+P +AAYA++
 Sbjct: 121 KRFFDGFPRNAHPMPVLSSVNALSAYYQDALPMDNGQVELSTIRLLAKLPTIAAYAYK 180

Query: 187 ARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTST 246
 G P++YPDNSL ENFLR+ FG+P EPY+ DP +V+ALD L ILHADHEQNCSTST
 Sbjct: 181 KSVGQPFLYPDNLTLVENFLRLTFGFPAPAEPYQADPEVVRALDMLFILHADHEQNCSTST 240

Query: 247 VRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEIDKNNHGGDATAFMNKVKNKE 306
 VR++GS++AN+F SI+GGINAL GPLHGGANQAVLEMLE I+++ G D + F+ KVKN+E
 Sbjct: 241 VRLVGSSRANLFTSISGGINALWGPLHGGANQAVLEMLEGIRDSD-GDDVSEFVRKVKNRE 299

Query: 307 DGVRLMGFHHRVYKNYDPRAAVKETAHEILEHXXXXXXXXXAIK-LEEIALADDYFISR 365
 GV+LMGFHHRVYKNYDPRA IVKE A +IL K LEE AL DDYFIR
 Sbjct: 300 AGVKLMGFHHRVYKNYDPRAIVKEQADKILAKLGDDSSLGIAKELEEAALTDDYFIER 359

Query: 366 KLYPNVDFTYTGLEYRAMGFTDFFTVLFAIGRLPGWIHYREQLGAAGNKINRPRQVYTG 425
 KLYPNVDFTYTGLEYRA+GFTP FTVLFA+GRLPGWI AH+RE +KI RPRQ+YTG
 Sbjct: 360 KLYPNVDFTYTGLEYRALGFPTRMFTVLALGRLPGWI AHWREMHDGDSKIGRPRQIYTG 419

Query: 426 KESRKLVPREER 437
 R V + R
 Sbjct: 420 YTERTDYVTIDAR 431

>tr:Q82CL5 [Q82CL5] Putative citrate synthase.>gpu:BA000030_5334 [BA000030] ▲Top
 putative citrate synthase [Streptomyces avermitilis
 MA-4680]>gp:AP005042_136 [AP005042] putative citrate
 synthase [Streptomyces avermitilis MA-4680]
 Length = 429

Score = 533 bits (1372), Expect = e-150
 Identities = 262/428 (61%), Positives = 325/428 (75%), Gaps = 2/428 (0%)

Query: 11 NNKAVLHYPGGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKITDG 70
 +N VL Y GE+ +I+++ G+ G +GK+ ++TGL+T D GY +T + +S ITY+DG
 Sbjct: 3 DNSVVLRYGDGEYTPVIDSTVGDKGFDIGKLRAQTGLVLDSGYGNATAYSITAITYLDG 62

Query: 71 DAGILRYRGYDIAADLAENATFNEVSYLLINGELPTPDELHKFNDEIRHHTLLDEDKSQF 130

+ GILRYRGY I LAE +TF EV+YLL INGELPT DEL F EI HTLL ED K+ +
 Sbjct: 63 EQGILRYRGYPIEQLAERSTFLEVAYLLINGELPTVDELSTFKGEITQHTLLHEDVKNFY 122

Query: 131 NVFPRDAHPMATLASSVNILSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAAYAHRAKG 190
 FPRDAHPMA L+S V+ LST+YQD NP DE Q + +T+RL+AK+P +AAAYA++ G
 Sbjct: 123 RGFPRDAHPMAMLSVSVSALSTFYQDSHNPFDEKQRNLSTIRLLAKLPTIAAYAYKKSIG 182

Query: 191 APYMPDSDLNARENFLRMFMGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTSTVRMI 250
 P++YP N L ENFLRM F P + Y++DP++V ALDKLLILHADHEQNCSTSTVR++
 Sbjct: 183 HPFVYPRNDLGYVENFLRMTFSVPAQDYDLDPVVVSALDKLLILHADHEQNCSTSTVRLV 242

Query: 251 GSAQANMFVSIAGGINALSGPLHGGGANQAVLEMLEDIKNHHGGDATAFMNKVKNKEDGVR 310
 GS+QANMF SI+ GI+AL GPLHGGANQ+VLEMLE I+ + GGD F+ KVKNKEDGV+
 Sbjct: 243 GSSQANMFASISAGISALWGPLHGGGANQSLEMLEGIQTSGGDVDTFIRKVKNKEDGVK 301

Query: 311 LMFGHHRVYKNYDPRAIVKETAHEILEH-XXXXXXXXXIKLEEIALADDYFISRKLKP 369
 LMFGHHRVYKN+DPRAI+K AH++L A+KLEE ALADDYF+ RKLKP
 Sbjct: 302 LMFGHHRVYKNFDPRAKIKAHHDVLSALGKSDELLDIALKLEEHALADDYFVERKLYP 361

Query: 370 NVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPROVYTGKESR 429
 NVDFYTGLIYRAMGFPT+FTVLFA+GRLPGWIA+E+G++I RPRQ+YTG+R
 Sbjct: 362 NVDFYTGLIYRAMGFTEMFTVLFALGRLPGWIAQWHEMIKEPGSRIGRPRQIYTGEVLR 421

Query: 430 KLPREER 437
 VP E R
 Sbjct: 422 DFVPVEGR 429

Database: nr-aa: Non-redundant protein sequence database Release
 05-01-04

Posted date: Jan 4, 2005 3:40 PM
 Number of letters in database: 600,567,511
 Number of sequences in database: 1,848,798

Lambda K H
 0.319 0.137 0.399

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 527,441,587
 Number of Sequences: 1848798
 Number of extensions: 22621601
 Number of successful extensions: 50691
 Number of sequences better than 10.0: 10
 Number of HSP's better than 10.0 without gapping: 665
 Number of HSP's successfully gapped in prelim test: 43
 Number of HSP's that attempted gapping in prelim test: 48255
 Number of HSP's gapped (non-prelim): 739

length of query: 437
 length of database: 600,567,511
 effective HSP length: 128
 effective length of query: 309
 effective length of database: 363,921,367
 effective search space: 112451702403
 effective search space used: 112451702403

T: 11
 A: 40
 X1: 16 (7.4 bits)
 X2: 38 (14.6 bits)
 X3: 64 (24.7 bits)

S1: 41 (21.7 bits)
S2: 75 (33.5 bits)

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